



Mo5176new.txt

<110> Bayer Aktiengesellschaft

<120> Nucleic Acids which encode
insect acetylcholine receptor subunits

<130> Le A 33 020-Foreign Countries

<140> US/09/303,232

<141> 1999-04-30

<150> DE 198 19 829.9

<151> 1998-05-04

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 2886

<212> DNA

<213> Drosophila melanogaster

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<221> CDS

<222> (372)..(2681)

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aaacaataaa gcatatactt gccatattga tataaaggga aatcgtgaaa aggcggtgaa 180

aatttcgtaa gattagttgg tattaaggc agcccatgca cacagctaaa aagggacta 240

aaaaaaacccc gcacagaaca atgaaagctg cagcagctgg ataaggccga caaaaccgaa 300

aattatatta ttgtatcta gtagagagca gacaacatat ccgctggcaa caaccaacac 360

cgaaagagac t atg aaa aat gca caa ctg aaa ctg act gaa gtt gac gat 410

Met Lys Asn Ala Gln Leu Lys Leu Thr Glu Val Asp Asp
1 5 10

gat gag ctg tgg ctg gca gta aga tta gcg cac tgc agc agc aac ttt 458
Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe
15 20 25

agc agc agt agc agc aca aga acc acc agc agc aac cag agg cac aac 506
Ser Ser Ser Ser Thr Arg Thr Ser Ser Asn Gln Arg His Asn
30 35 40 45

cag caa ctc aca aca ctg caa cca agg agc tta agt aca aaa cac cac 554
Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His
50 55 60

agc aac att gca agc gag cag cac aat agc cag caa cag gag cca gca 602
Ser Asn Ile Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala
65 70 75

tcg aag gac gag gat gta gcc aac cac ggt aga agc aat gac cag cag 650
Ser Lys Asp Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln
80 85 90

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acg cat ctg caa cag cta gac agc agc aac atg ttg tcg cca aag aca	698
Thr His Leu Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr	
95 100 105	
gcc gca gca gca act gct gcc ggc gat gaa gca aca acc caa caa cca	746
Ala Ala Ala Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro	
110 115 120 125	
aca aac ata aga ctg tgt gca cgc aag cga caa cga ttg cgt cgc cga	794
Thr Asn Ile Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg	
130 135 140	
cga aaa aga aaa cca gca acc cca aac gaa aca gat atc aag aaa caa	842
Arg Lys Arg Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln	
145 150 155	
cag caa ctt agc atg cct ccc ttc aaa acg cgc aaa tcc acg gac acc	890
Gln Gln Leu Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr	
160 165 170	
tac agc aca cca gca aca acc agc tgt ccg aca gcc acc tac atg	938
Tyr Ser Thr Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met	
175 180 185	
caa tgt cga gcc agc gac aat gag ttc agt att ccg ata tcg aga cat	986
Gln Cys Arg Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His	
190 195 200 205	
gat aga gta tcc acg gcc aca ttc gcc tgg gtg ttg cat gtg ctg cag	1034
Asp Arg Val Ser Thr Ala Thr Phe Ala Trp Val Leu His Val Leu Gln	
210 215 220	
gtg ctg ctc gtg tcg ctg caa cag tgg caa ctt cac gtg caa cag cga	1082
Val Leu Leu Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg	
225 230 235	
tcg gtg cta ctg ttc aga agg atc gca gcg agc acc atc gcc ttc att	1130
Ser Val Leu Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile	
240 245 250	
tcc tat tta ggc agc ttt gca gcg caa ctg aaa aat agc agc agc agc	1178
Ser Tyr Leu Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser	
255 260 265	
agt agc agc agc aac agc agc aac aac agc agc agc caa ata tta aac	1226
Ser Ser Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn	
270 275 280 285	
gga ctt aat aaa cac tca tgg ata ttt tta ttg ata tat ttg aat tta	1274
Gly Leu Asn Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu	
290 295 300	
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Ser Ala Lys Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His	
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gat ctt ttg gat cct tat aat aca cta gaa cgt ccc gtt ctc aat gaa	1370
Asp Leu Leu Asp Pro Tyr Asn Thr Leu Glu Arg Pro Val Leu Asn Glu	
320 325 330	
tcg gac ccg tta caa tta agc ttt ggt tta act tta atg caa att atc	1418
Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile	

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335

340

345

gat	gtg	gac	gag	aaa	aat	caa	ttg	cta	gtc	act	aat	gtg	tgg	tta	aaa	1466
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Leu	Glu	Trp	Asn	Asp	Met	Asn	Leu	Arg	Trp	Asn	Thr	Ser	Asp	Tyr	Gly	
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Gly	Val	Lys	Asp	Leu	Arg	Ile	Pro	Pro	His	Arg	Ile	Trp	Lys	Pro	Asp	
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gtg	ctg	atg	tac	aac	agt	gcg	gat	gag	gga	ttt	gac	ggc	acc	tac	cag	1610
Val	Leu	Met	Tyr	Asn	Ser	Ala	Asp	Glu	Gly	Phe	Asp	Gly	Thr	Tyr	Gln	
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Thr	Asn	Val	Val	Val	Arg	Asn	Asn	Gly	Ser	Cys	Leu	Tyr	Val	Pro	Pro	
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Gly	Ile	Phe	Lys	Ser	Thr	Cys	Lys	Ile	Asp	Ile	Thr	Trp	Phe	Pro	Phe	
		430				435					440			445		
gat	gac	cag	cg	tgc	gag	atg	aag	ttc	ggc	agt	tgg	acc	tac	gac	gga	1754
Asp	Asp	Gln	Arg	Cys	Glu	Met	Lys	Phe	Gly	Ser	Trp	Thr	Tyr	Asp	Gly	
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Phe	Gln	Leu	Asp	Leu	Gln	Leu	Gln	Asp	Glu	Thr	Gly	Gly	Asp	Ile	Ser	
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Ser	Tyr	Val	Leu	Asn	Gly	Glu	Trp	Glu	Leu	Leu	Gly	Val	Pro	Gly	Lys	
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cgt	aac	gag	atc	tat	ta	cc	aac	tgc	tgc	ccg	gaa	ccc	tat	ata	gac	1898
Arg	Asn	Glu	Ile	Tyr	Tyr	Asn		Cys	Cys	Pro	Glu	Pro	Tyr	Ile	Asp	Ile
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Thr	Phe	Ala	Ile	Ile	Ile	Arg	Arg	Arg	Arg	Thr	Leu	Tyr	Tyr	Phe	Phe	
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ctg	atc	ata	cct	tgt	gta	ctg	att	gcc	tcc	atg	gcc	ttg	ctc	gga	ttc	1994
Leu	Ile	Ile	Pro	Cys	Val	Leu	Ile	Ala	Ser	Met	Ala	Leu	Leu	Gly	Phe	
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acc	ctg	ccg	cca	gat	tcg	ggt	gaa	aaa	tta	tcg	ctg	ggt	gtt	acc	atc	2042
Thr	Leu	Pro	Pro	Asp	Ser	Gly	Glu	Lys	Leu	Ser	Leu	Gly	Val	Thr	Ile	
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ttg	ctc	tcg	ctg	acc	gtg	ttt	ctg	aat	atg	gtt	gcc	gag	aca	atg	ccg	2090
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gct	act	tcc	gat	g	gt	cc	tt	tg	ta	cg	atc	gt	ttt	tt	tg	2138
Ala	Thr	Ser	Asp	Ala	Val	Pro	Leu	Trp	Ile	Arg	Ile	Val	Phe	Leu	Cys	
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<213> *Drosophila melanogaster*

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Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe Ser Ser Ser
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Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn Gln Gln Leu
35 40 45

Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His Ser Asn Ile
50 55 60

Ala Ser Glu Gln His Asn Ser Gln Gln Glu Pro Ala Ser Lys Asp
65 70 75 80

Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln Thr His Leu
85 90 95

Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr Ala Ala Ala
100 105 110

Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro Thr Asn Ile
115 120 125

Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg Arg Lys Arg
130 135 140

Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln Gln Gln Leu
145 150 155 160

Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr Tyr Ser Thr
165 170 175

Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met Gln Cys Arg
180 185 190

Ala Ser Asp Asn Glu Phe Ser Ile Pro Ile Ser Arg His Asp Arg Val
195 200 205

Ser Thr Ala Thr Phe Ala Trp Val Leu His Val Leu Gln Val Leu Leu
210 215 220

Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg Ser Val Leu
225 230 235 240

Leu Phe Arg Arg Ile Ala Ala Ser Thr Ile Ala Phe Ile Ser Tyr Leu
245 250 255

Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser Ser Ser Ser
260 265 270

Ser Asn Ser Ser Asn Asn Ser Ser Thr Gln Ile Leu Asn Gly Leu Asn
275 280 285

Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu Ser Ala Lys
290 295 300

Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His Asp Leu Leu
305 310 315 320

Asp Pro Tyr Asn Thr Leu Glu Arg Pro Val Leu Asn Glu Ser Asp Pro
325 330 335

Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile Asp Val Asp
340 345 350

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Glu Lys Asn Gln Leu Leu Val Thr Asn Val Trp Leu Lys Leu Glu Trp
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Asn Asp Met Asn Leu Arg Trp Asn Thr Ser Asp Tyr Gly Gly Val Lys
 370 375 380

Asp Leu Arg Ile Pro Pro His Arg Ile Trp Lys Pro Asp Val Leu Met
 385 390 395 400

Tyr Asn Ser Ala Asp Glu Gly Phe Asp Gly Thr Tyr Gln Thr Asn Val
 405 410 415

Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro Gly Ile Phe
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Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe Asp Asp Gln
 435 440 445

Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Phe Gln Leu
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Asp Leu Gln Leu Gln Asp Glu Thr Gly Gly Asp Ile Ser Ser Tyr Val
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Leu Asn Gly Glu Trp Glu Leu Leu Gly Val Pro Gly Lys Arg Asn Glu
 485 490 495

Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile Thr Phe Ala
 500 505 510

Ile Ile Ile Arg Arg Arg Thr Leu Tyr Tyr Phe Phe Asn Leu Ile Ile
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Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe Thr Leu Pro
 530 535 540

Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile Leu Leu Ser
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Leu Thr Val Phe Leu Asn Met Val Ala Glu Thr Met Pro Ala Thr Ser
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Asp Ala Val Pro Leu Trp Ile Arg Ile Val Phe Leu Cys Trp Leu Pro
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Trp Ile Leu Arg Met Ser Arg Pro Gly Arg Pro Leu Ile Leu Glu Phe
 595 600 605

Pro Thr Thr Pro Cys Ser Asp Thr Ser Ser Glu Arg Lys His Gln Ile
 610 615 620

Leu Ser Asp Val Glu Leu Lys Glu Arg Ser Ser Lys Ser Leu Leu Ala
 625 630 635 640

Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Asn Cys Arg Pro Met
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Thr Pro Gly Gly Thr Leu Pro His Asn Pro Ala Phe Tyr Arg Thr Val
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Tyr Gly Gln Gly Asp Asp Gly Ser Ile Gly Pro Ile Gly Ser Thr Arg
 675 680 685

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Met Pro Asp Ala Val Thr His His Thr Cys Ile Lys Ser Ser Thr Glu
690 695 700

Tyr Glu Leu Gly Leu Ile Leu Lys Glu Ile Arg Phe Ile Thr Asp Gln
705 710 715 720

Leu Arg Lys Asp Asp Glu Cys Asn Asp Ile Ala Asn Asp Trp Lys Phe
725 730 735

Ala Ala Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe Thr Met Phe
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Val Ser
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gcggcgcgcg ggcgcggcgc tgac atg gac ggg cgg gcg cgc cgc 355
Met Gly Gly Arg Ala Arg Arg
1 5

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Ser His Leu Ala Ala Pro Ala Gly Leu Leu Leu Leu Leu Cys Leu Leu
10 15 20

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Trp Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His
25 30 35

cac cta ttg gac cac tac aac gta ctg gag agg ccc gtc gtc aac gag 499
His Leu Leu Asp His Tyr Asn Val Leu Glu Arg Pro Val Val Asn Glu
40 45 50 55

agc gac ccg ctg cag ctc tcc ttc ggc ctc acg ctc atg cag atc atc 547
Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile
60 65 70

gac gtg gac gag aag aac cag ctt tta ata aca aac atc tgg cta aaa 595
Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Lys
75 80 85

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90 95 100	
ggg gtc aaa gat tta aga gtg cca ccc cac aga cta tgg aaa cca gac	691
Gly Val Lys Asp Leu Arg Val Pro Pro His Arg Leu Trp Lys Pro Asp	
105 110 115	
gtc ctt atg tac aac agc gcg gac gaa ggg ttc gac agc acg tat cca	739
Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe Asp Ser Thr Tyr Pro	
120 125 130 135	
acg aac gtg gtg cgg aac aac ggc tcg tgt ctg tac gtg ccg ccc	787
Thr Asn Val Val Arg Asn Asn Gly Ser Cys Leu Tyr Val Pro Pro	
140 145 150	
ggc atc ttc aag agc acc tgc aag atc gac atc acc tgg ttc ccc ttc	835
Gly Ile Phe Lys Ser Thr Cys Lys Ile Asp Ile Thr Trp Phe Pro Phe	
155 160 165	
gac gac caa cga tgc gag atg aag ttt ggc agc tgg act tat gat ggt	883
Asp Asp Gln Arg Cys Glu Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly	
170 175 180	
tat cag ttg gat cta caa cta cag gat gaa ggg ggc gga gat ata agc	931
Tyr Gln Leu Asp Leu Gln Leu Gln Asp Glu Gly Gly Asp Ile Ser	
185 190 195	
agt ttt gtc acg aat ggc gaa tgg gag tta ata gga gtc ccc ggc aag	979
Ser Phe Val Thr Asn Gly Glu Trp Glu Leu Ile Gly Val Pro Gly Lys	
200 205 210 215	
cgc aac gag atc tac tac aac tgt tgt ccg gag cca tac atc gac atc	1027
Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Pro Tyr Ile Asp Ile	
220 225 230	
acg ttt gcg gtg gtg atc cgg agg aaa acg ctc tac tac ttc ttc aat	1075
Thr Phe Ala Val Val Ile Arg Arg Lys Thr Leu Tyr Tyr Phe Phe Asn	
235 240 245	
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Leu Ile Val Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe	
250 255 260	
acc ttg cct cca gac tcc gga gaa aag ttg tct tta ggt gtg acg ata	1171
Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Ser Leu Gly Val Thr Ile	
265 270 275	
tta ctg tcg ttg acg gtg ttc ctc aac atg gtg gcg gag acg atg cca	1219
Leu Leu Ser Leu Thr Val Phe Leu Asn Met Val Ala Glu Thr Met Pro	
280 285 290 295	
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Ala Thr Ser Asp Ala Val Pro Leu Leu Gly Thr Tyr Phe Asn Cys Ile	
300 305 310	
atg ttc atg gtg gct tcc tcc gtc gtc tcc acc ata ctg atc ctc aac	1315
Met Phe Met Val Ala Ser Ser Val Val Ser Thr Ile Leu Ile Leu Asn	
315 320 325	
tac cac cac cgg cac gca gac act cac gaa atg agt gat tgg att cgt	1363
Tyr His His Arg His Ala Asp Thr His Glu Met Ser Asp Trp Ile Arg	

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tgc	gtg	ttc	ctt	tat	tgg	ctg	ccg	tgg	gtg	ctg	cgc	atg	tca	cg	ccc	1411
Cys	Val	Phe	Leu	Tyr	Trp	Leu	Pro	Trp	Val	Leu	Arg	Met	Ser	Arg	Pro	
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Gly	Ser	Ala	Thr	Thr	Pro	Pro	Pro	Ala	Arg	Val	Pro	Pro	Pro	Pro	Asp	
360					365					370					375	
ctg	gag	ctg	cgc	gag	cgc	tcc	tcc	aag	tgc	ctc	cta	g	aac	gtg	ctc	1507
Leu	Glu	Leu	Arg	Glu	Arg	Ser	Ser	Lys	Ser	Leu	Leu	Ala	Asn	Val	Leu	
					380				385					390		
gac	atc	gat	gac	gac	ttc	cgc	cac	ccg	caa	g	cg	cag	cag	ccg	caa	1555
Asp	Ile	Asp	Asp	Asp	Phe	Arg	His	Pro	Gln	Ala	Gln	Gln	Pro	Gln	Cys	
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tgc	cga	ta	ca	agg	ggg	gg	gag	gag	aat	ggc	g	gg	tt	g	g	1603
Cys	Arg	Tyr	Tyr	Arg	Gly	Gly	Glu	Glu	Asn	Gly	Ala	Gly	Leu	Ala	Ala	
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cac	agt	tc	ttc	gg	gtc	gac	ta	ca	gg	ctc	tc	tc	at	ctg	aag	1651
His	Ser	Cys	Phe	Gly	Val	Asp	Tyr	Glu	Leu	Ser	Leu	Ile	Leu	Lys	Glu	
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att	aga	gtc	atc	aca	gat	cag	atg	cgc	aag	gac	gac	gaa	gat	g	g	1699
Ile	Arg	Val	Ile	Thr	Asp	Gln	Met	Arg	Lys	Asp	Asp	Glu	Asp	Ala	Asp	
					440		445		450					455		
att	tcg	cgc	gac	tgg	aag	ttc	gcc	gcc	atg	gtc	gt	gac	aga	ctg	tc	1747
Ile	Ser	Arg	Asp	Trp	Lys	Phe	Ala	Ala	Met	Val	Val	Asp	Arg	Leu	Cys	
					460			465			470					
ctt	att	atc	ttt	acc	ctg	ttc	aca	atc	atc	gcc	ac	ct	g	gt	ct	1795
Leu	Ile	Ile	Phe	Thr	Leu	Phe	Thr	Ile	Ile	Ala	Thr	Leu	Ala	Val	Leu	
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ctg	tcc	g	cc	cc	ac	ac	atc	atg	gt	tc	tagc	gac	cc	cc	tttgc	1842
Leu	Ser	Ala	Pro	His	Ile	Met	Val	Ser								
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tgg	cg	gg	ac	g	gt	gac	ccg	gg	tt	g	cc	c	tt	cc	cc	1962
ccc	ct	tt	tt	aa	ta	at	cc	cc	tt	cc	cc	cc	tt	tt	cc	2022
atcc	gact	aa	tttt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	2082
agaata	ca	aa	at	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	2142
tat	ttcc	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	2202
ccgg	aa	cc	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	2262
ccac	gg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2322
ggcc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	2382
ccgat	ga	ac	ctg	att	cg	at	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	2442
aat	ctt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	2502

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cgaaaattta ttcaaaacaga tgcgaccatc gtttcaaaaca tttacatgtt atatagaact 2922
cattttataa gatataacaac attttataag tacaagaagt tgtaacatgtt accgggtttt 2982
cgttacatag agggtataac acaaagggtgc ctacatattt acagatgcga agcacgatca 3042
gttataagc acaggtacac tatacctga catccgacag tcctgcccct cgtctgccac 3102
actcggaaac attcgacagt tcagttact gctccgccat catcgattgt taagttgtt 3162
gttctaactc atcgcattca tttcattcaa aaacattgtt aaccctctcaa ggggaaaacg 3222
tgggttaaac agtgagagtg cgccgggtaca accgacacgc gaatgtaccc tcgcaaggct 3282
cctgtatgt tttcctttc cgaggtgtt ctgagagtaa tcttagacgg tccgatggaa 3342
gttgcggacc ggatatgatt acaagtcaat gtttttaagt catccgttta tttattgtt 3402
tatcttctta ccattcgctt gaggtgtgtt gacgacccgg acgggtggcg ccgcaacccg 3462
cacacgcggg gttccatctt tgtatttagat ggaagttgtt cggcatctt ccgtcggcaa 3522
tgggacaacc cggtgtcccc aacattgtt caattgttag ggttaactctt gaattgcact 3582
ttgtttatta aatataaacg aatgaaaaca aaaaaaaaaaaa aaaaaactcg agagtacttc 3642
tagagcggcc gcgggcccattt cgattttcca cccgggtggg gtaccagtaa gtgtaccc 3700

<210> 4
<211> 496
<212> PRT
<213> Heliothis virescens

<400> 4
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Leu Leu Leu Leu Cys Leu Leu Trp Pro Arg Gly Ala Arg Cys Gly Tyr
20 25 30
His Glu Lys Arg Leu Leu His His Leu Leu Asp His Tyr Asn Val Leu
35 40 45
Glu Arg Pro Val Val Asn Glu Ser Asp Pro Leu Gln Leu Ser Phe Gly
50 55 60
Leu Thr Leu Met Gln Ile Ile Asp Val Asp Glu Lys Asn Gln Leu Leu
65 70 75 80

Mo5176new.txt

Ile Thr Asn Ile Trp Leu Lys Leu Glu Trp Asn Asp Met Asn Leu Arg
85 90 95

Trp Asn Thr Ser Asp Phe Gly Gly Val Lys Asp Leu Arg Val Pro Pro
100 105 110

His Arg Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu
115 120 125

Gly Phe Asp Ser Thr Tyr Pro Thr Asn Val Val Arg Asn Asn Gly
130 135 140

Ser Cys Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Ile
145 150 155 160

Asp Ile Thr Trp Phe Pro Phe Asp Asp Gln Arg Cys Glu Met Lys Phe
165 170 175

Gly Ser Trp Thr Tyr Asp Gly Tyr Gln Leu Asp Leu Gln Leu Gln Asp
180 185 190

Glu Gly Gly Asp Ile Ser Ser Phe Val Thr Asn Gly Glu Trp Glu
195 200 205

Leu Ile Gly Val Pro Gly Lys Arg Asn Glu Ile Tyr Tyr Asn Cys Cys
210 215 220

Pro Glu Pro Tyr Ile Asp Ile Thr Phe Ala Val Val Ile Arg Arg Lys
225 230 235 240

Thr Leu Tyr Tyr Phe Phe Asn Leu Ile Val Pro Cys Val Leu Ile Ala
245 250 255

Ser Met Ala Leu Leu Gly Phe Thr Leu Pro Pro Asp Ser Gly Glu Lys
260 265 270

Leu Ser Leu Gly Val Thr Ile Leu Leu Ser Leu Thr Val Phe Leu Asn
275 280 285

Met Val Ala Glu Thr Met Pro Ala Thr Ser Asp Ala Val Pro Leu Leu
290 295 300

Gly Thr Tyr Phe Asn Cys Ile Met Phe Met Val Ala Ser Ser Val Val
305 310 315 320

Ser Thr Ile Leu Ile Leu Asn Tyr His His Arg His Ala Asp Thr His
325 330 335

Glu Met Ser Asp Trp Ile Arg Cys Val Phe Leu Tyr Trp Leu Pro Trp
340 345 350

Val Leu Arg Met Ser Arg Pro Gly Ser Ala Thr Thr Pro Pro Pro Ala
355 360 365

Arg Val Pro Pro Pro Asp Leu Glu Leu Arg Glu Arg Ser Ser Lys
370 375 380

Ser Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Pro
385 390 395 400

Gln Ala Gln Gln Pro Gln Cys Cys Arg Tyr Tyr Arg Gly Gly Glu Glu
405 410 415

Mo5176new.txt

Asn Gly Ala Gly Leu Ala Ala His Ser Cys Phe Gly Val Asp Tyr Glu
 420 425 430
 Leu Ser Leu Ile Leu Lys Glu Ile Arg Val Ile Thr Asp Gln Met Arg
 435 440 445
 Lys Asp Asp Glu Asp Ala Asp Ile Ser Arg Asp Trp Lys Phe Ala Ala
 450 455 460
 Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe Thr Leu Phe Thr Ile
 465 470 475 480
 Ile Ala Thr Leu Ala Val Leu Leu Ser Ala Pro His Ile Met Val Ser
 485 490 495

<210> 5
 <211> 3109
 <212> DNA
 <213> Heliothis virescens

<220>
 <221> CDS
 <222> (95)..(1597)

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 Met Ala Pro Met Leu Ala Ala
 1 5
 ttg gcg ctg ctg gct ttg ctg ccc gta tcg gag caa ggt cct cac gag 163
 Leu Ala Leu Ala Leu Leu Pro Val Ser Glu Gln Gly Pro His Glu
 10 15 20
 aag aga ctc ctg aac gcg ttg ctg gcg aac tac aac acc ctg gag cga 211
 Lys Arg Leu Leu Asn Ala Leu Leu Ala Asn Tyr Asn Thr Leu Glu Arg
 25 30 35
 ccg gtg gcc aac gag agc gaa ccg cta gag gtc agg ttc ggc ttg acc 259
 Pro Val Ala Asn Glu Ser Glu Pro Leu Glu Val Arg Phe Gly Leu Thr
 40 45 50 55
 ttg cag caa atc att gac gtg gac gag aag aat caa cta ctt ata acc 307
 Leu Gln Gln Ile Ile Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr
 60 65 70
 aat ata tgg ctg tcg ttg gag tgg aat gac tac aac ctg agg tgg aac 355
 Asn Ile Trp Leu Ser Leu Glu Trp Asn Asp Tyr Asn Leu Arg Trp Asn
 75 80 85
 gac agc gag tat ggc ggg gtc aag gac ctc agg atc acg ccc aac aag 403
 Asp Ser Glu Tyr Gly Gly Val Lys Asp Leu Arg Ile Thr Pro Asn Lys
 90 95 100
 ttg tgg aag ccg gac gtc ctt atg tat aat agt gct gac gag ggt ttt 451
 Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe
 105 110 115
 gac ggg acc tac cag acc aac gtg gtg gtc aga agc ggc ggc agt tgc 499
 Asp Gly Thr Tyr Gln Thr Asn Val Val Val Arg Ser Gly Gly Ser Cys

Mo5176new.txt

120	125	130	135	
ctg tac gtg cca cct ggc ata ttc aag agc aca tgc aag atg gac atc Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Met Asp Ile 140 145 150				547
gcg tgg ttt ccc ttc gac gac caa cac tgt gat atg aag ttc ggt agc Ala Trp Phe Pro Phe Asp Asp Gln His Cys Asp Met Lys Phe Gly Ser 155 160 165				595
tgg aca tat gac ggc aat cag ttg gat ctg gtg cta aaa gat gag gca Trp Thr Tyr Asp Gly Asn Gln Leu Asp Leu Val Leu Lys Asp Glu Ala 170 175 180				643
ggc ggc gat cta tcg gac ttc ata aca aat ggg gag tgg tat cta ata Gly Gly Asp Leu Ser Asp Phe Ile Thr Asn Gly Glu Trp Tyr Leu Ile 185 190 195				691
gga atg cca ggc aaa aag aac aca ata aca tac gcg tgc tgc ccc gag Gly Met Pro Gly Lys Lys Asn Thr Ile Thr Tyr Ala Cys Cys Pro Glu 200 205 210 215				739
ccc tac gtg gac gtc acc ttc acc atc atg ata aga aga cga acc ttg Pro Tyr Val Asp Val Thr Phe Thr Ile Met Ile Arg Arg Arg Thr Leu 220 225 230				787
tac tac ttc ttc aac ctg atc gtc ccg tgc gtg ctg atc tca tcg atg Tyr Tyr Phe Asn Leu Ile Val Pro Cys Val Leu Ile Ser Ser Met 235 240 245				835
gca ctc ctc ggc ttc aca ctg cca cca gac tcc gga gag aaa ctc aca Ala Leu Leu Gly Phe Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Thr 250 255 260				883
ctt gga gtc act att ctt cta tcg ctg acg gtg ttc ctc aac ctg gta Leu Gly Val Thr Ile Leu Leu Ser Leu Thr Val Phe Leu Asn Leu Val 265 270 275				931
gcc gag acc ctg cca cag gtc tcc gac gct atc ccc ctg tta ggg acg Ala Glu Thr Leu Pro Gln Val Ser Asp Ala Ile Pro Leu Leu Gly Thr 280 285 290 295				979
tac ttc aat tgc atc atg ttc atg gta gcg tcg tct gtg gta ctg act Tyr Phe Asn Cys Ile Met Phe Met Val Ala Ser Ser Val Val Leu Thr 300 305 310				1027
gtg gtg gta ctc aat tac cac cat cga aca gct gat ata cat gaa atg Val Val Val Leu Asn Tyr His His Arg Thr Ala Asp Ile His Glu Met 315 320 325				1075
cca cag tgg ata aaa tca gta ttc cta caa tgg ttg cca tgg ata ctg Pro Gln Trp Ile Lys Ser Val Phe Leu Gln Trp Leu Pro Trp Ile Leu 330 335 340				1123
cga atg tcg agg cca ggg aag aag atc acc agg aag act ata atg atg Arg Met Ser Arg Pro Gly Lys Lys Ile Thr Arg Lys Thr Ile Met Met 345 350 355				1171
aac acg agg atg agg gag ctg gaa ctg aag gag agg tcg tcg aag tcc Asn Thr Arg Met Arg Glu Leu Glu Leu Lys Glu Arg Ser Ser Lys Ser 360 365 370 375				1219
ttg ctg gcg aat gtt cta gat att gat gat gac ttc aga cac ggc cct				1267

Mo5176new.txt

Leu	Leu	Ala	Asn	Val	Leu	Asp	Ile	Asp	Asp	Asp	Phe	Arg	His	Gly	Pro	
380					385								390			
ccg	cct	cct	aac	agt	act	gcc	tcg	acc	ggg	aat	ttg	gga	cct	ggg	tgc	1315
Pro	Pro	Pro	Asn	Ser	Thr	Ala	Ser	Thr	Gly	Asn	Leu	Gly	Pro	Gly	Cys	
395					400								405			
tca	ata	ttc	cgc	acg	gat	ttc	cgt	cgg	tcg	ttc	gtc	cgt	ccg	tcc	acg	1363
Ser	Ile	Phe	Arg	Thr	Asp	Phe	Arg	Arg	Ser	Phe	Val	Arg	Pro	Ser	Thr	
410		415									420					
atg	gaa	gac	gtg	ggc	ggc	ggg	ctg	ggt	agc	cac	cat	cgc	gag	ctg	cac	1411
Met	Glu	Asp	Val	Gly	Gly	Gly	Leu	Gly	Ser	His	His	Arg	Glu	Leu	His	
425				430						435						
ctc	ata	ctg	aga	gag	ctg	cag	ttc	atc	acg	gcc	agg	atg	aag	aag	gct	1459
Leu	Ile	Leu	Arg	Glu	Leu	Gln	Phe	Ile	Thr	Ala	Arg	Met	Lys	Lys	Ala	
440		445						450					455			
gat	gag	gaa	gcc	gag	ctg	atc	agc	gac	tgg	aag	ttt	gct	gcg	atg	gtt	1507
Asp	Glu	Glu	Ala	Glu	Leu	Ile	Ser	Asp	Trp	Lys	Phe	Ala	Ala	Met	Val	
460				465						470						
gtt	gat	agg	ttt	tgc	ctg	ttc	gtg	ttc	aca	ctt	ttc	aca	atc	atc	gct	1555
Val	Asp	Arg	Phe	Cys	Leu	Phe	Val	Phe	Thr	Leu	Phe	Thr	Ile	Ile	Ala	
475				480						485						
aca	gta	gct	gtc	ctg	tta	tcg	gca	ccg	cat	atc	atc	gtg	caa			1597
Thr	Val	Ala	Val	Leu	Leu	Ser	Ala	Pro	His	Ile	Ile	Val	Gln			
490				495						500						
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ccgatttgt	attataattg	ataatgtat	taaattaaat	acgtgggtga	aacgcacacg											1717
tctccataac	aaagtcttaa	gacattaaat	tatgataaaat	ttacatattg	tagttaagtc											1777
gagtgttgc	ggaaatttta	gccggcgcaa	ggagttcgt	gaaggtctgt	atatatattt											1837
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ttaaacaat	gtgatgttga	ctaggatgtt	atacagataa	atgttgacgt	gtataattt											2017
ttaaaataaa	caatattaaat	tactattact	aaacgatatt	ataaacgaag	tactaacgag											2077
ggttacttta	atggaaagaa	cgctaagctg	gcacagagg	gcattaattt	aaaaaaagaa											2137
attacggaaa	aaagtttatt	gaaaattgaa	ctttttggaa	ggaaagtaac	gtttgatcaa											2197
aaaagtttgc	aaaacgaaag	ttcggttctg	cgcataact	ggaattaaaa	ttctcgtaaa											2257
tattaggaa	aagaagg	tcc	tttaaaacaa	aagatttga	ccggcatcct	ttttacaagt										2317
aatgagggat	cacagatgt	gacaaaaaac	cttagggat	ataagtaatg	tacataatgg											2377
atcaaatac	ggttagtgc	agaatgtt	acgat	tttgcataat	tcgatattaa											2437
aattcgat	gctgttgc	ctgcgttac	tttgatacat	atcgat	atcgatattt											2497
tataaattt	gatagatcg	acattagtaa	tgagtatg	gca	tttttaattt	tttaaaaaag										2557

aatgtactac gaagattaaa tccaggaatt gttaaacagt tatggaattt ataagaaatc 2617
 aacaattaat acggaaccaa aggtagacta ggtgttagcat caggagattt aattaaaaca 2677
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 ctcattgtcg attaaatgga gaataacttt tgatctctcg tatcgataaa tgctcactta 2797
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 tcagaaatag tcattaatta ggaatcggtt tgtgttaatg ttatgcttag cgaaaatatt 2917
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 tattgcgtg tgtatggta tataaatttt agaaaaaaaaaaaaaaa aactcgagag 3037
 tacttctaga gcggccgcgg gcccattcgat tttccacccg ggtgggtac caggttaagt 3097
 tacccaaattc gc

3109

<210> 6
 <211> 501
 <212> PRT
 <213> *Heliothis virescens*

<400> 6
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 Ser Glu Gln Gly Pro His Glu Lys Arg Leu Leu Asn Ala Leu Leu Ala
 20 25 30
 Asn Tyr Asn Thr Leu Glu Arg Pro Val Ala Asn Glu Ser Glu Pro Leu
 35 40 45
 Glu Val Arg Phe Gly Leu Thr Leu Gln Gln Ile Ile Asp Val Asp Glu
 50 55 60
 Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Ser Leu Glu Trp Asn
 65 70 75 80
 Asp Tyr Asn Leu Arg Trp Asn Asp Ser Glu Tyr Gly Gly Val Lys Asp
 85 90 95
 Leu Arg Ile Thr Pro Asn Lys Leu Trp Lys Pro Asp Val Leu Met Tyr
 100 105 110
 Asn Ser Ala Asp Glu Gly Phe Asp Gly Thr Tyr Gln Thr Asn Val Val
 115 120 125
 Val Arg Ser Gly Gly Ser Cys Leu Tyr Val Pro Pro Gly Ile Phe Lys
 130 135 140
 Ser Thr Cys Lys Met Asp Ile Ala Trp Phe Pro Phe Asp Asp Gln His
 145 150 155 160
 Cys Asp Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Asn Gln Leu Asp
 165 170 175
 Leu Val Leu Lys Asp Glu Ala Gly Gly Asp Leu Ser Asp Phe Ile Thr
 180 185 190

Mo5176new.txt

Asn Gly Glu Trp Tyr Leu Ile Gly Met Pro Gly Lys Lys Asn Thr Ile
 195 200 205

Thr Tyr Ala Cys Cys Pro Glu Pro Tyr Val Asp Val Thr Phe Thr Ile
 210 215 220

Met Ile Arg Arg Arg Thr Leu Tyr Tyr Phe Phe Asn Leu Ile Val Pro
 225 230 235 240

Cys Val Leu Ile Ser Ser Met Ala Leu Leu Gly Phe Thr Leu Pro Pro
 245 250 255

Asp Ser Gly Glu Lys Leu Thr Leu Gly Val Thr Ile Leu Leu Ser Leu
 260 265 270

Thr Val Phe Leu Asn Leu Val Ala Glu Thr Leu Pro Gln Val Ser Asp
 275 280 285

Ala Ile Pro Leu Leu Gly Thr Tyr Phe Asn Cys Ile Met Phe Met Val
 290 295 300

Ala Ser Ser Val Val Leu Thr Val Val Val Leu Asn Tyr His His Arg
 305 310 315 320

Thr Ala Asp Ile His Glu Met Pro Gln Trp Ile Lys Ser Val Phe Leu
 325 330 335

Gln Trp Leu Pro Trp Ile Leu Arg Met Ser Arg Pro Gly Lys Lys Ile
 340 345 350

Thr Arg Lys Thr Ile Met Met Asn Thr Arg Met Arg Glu Leu Glu Leu
 355 360 365

Lys Glu Arg Ser Ser Lys Ser Leu Leu Ala Asn Val Leu Asp Ile Asp
 370 375 380

Asp Asp Phe Arg His Glu Pro Pro Pro Pro Asn Ser Thr Ala Ser Thr
 385 390 395 400

Gly Asn Leu Gly Pro Gly Cys Ser Ile Phe Arg Thr Asp Phe Arg Arg
 405 410 415

Ser Phe Val Arg Pro Ser Thr Met Glu Asp Val Gly Gly Leu Gly
 420 425 430

Ser His His Arg Glu Leu His Leu Ile Leu Arg Glu Leu Gln Phe Ile
 435 440 445

Thr Ala Arg Met Lys Lys Ala Asp Glu Glu Ala Glu Leu Ile Ser Asp
 450 455 460

Trp Lys Phe Ala Ala Met Val Val Asp Arg Phe Cys Leu Phe Val Phe
 465 470 475 480

Thr Leu Phe Thr Ile Ile Ala Thr Val Ala Val Leu Leu Ser Ala Pro
 485 490 495

His Ile Ile Val Gln
 500

Mo5176new.txt

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<212> DNA
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<220>
<221> modified_base
<222> (6)
<223> i

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20

<210> 8
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<220>
<221> modified_base
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<223> i

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20

<210> 9
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>212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
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32

<210> 10
<211> 27
>212> DNA
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<220>
<223> Primer

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27

<210> 11
<211> 41
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<220>
<223> Primer

Mo5176new.txt

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<220>
<223> Primer

<400> 12
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<210> 13
<211> 27
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<220>
<223> Primer

<400> 13
gcaagcgccg ctatggcccc tatgttg 27

<210> 14
<211> 29
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<220>
<223> Primer

<400> 14
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